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ANALYSIS OF DIVERGENCE IN SOME COLD-TOLERANT RICES

R. N. KAW*

Department of Plant Breeding, International Rice Research Institute
P.O. Box 933, Manila, Philippines

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ABSTRACT

Genetic divergence of ninety-four rice genotypes, comprising 74 F$_1$s and 20 parents, grown over three cold stress environments, was assessed based on five reproductive stage cold tolerance and adaptability related characters. Using D^2 statistic and canonical analyses, the genotypes were grouped into 18 clusters. The clustering pattern suggested that genetic and geographic diversity were not necessarily related. Plant height, days to flowering, fertile spikelets/panicle and percent fertility were indicated as important contributors to genetic divergence in cold tolerant rices. Traditional japonica varieties and their *japonica* x *indica* hybrids were distinctly apart from the *indica* varieties and *indica* x *indica* hybrids in the analyses. The divergence of *japonica* cultivars K332 and Barkat, and the *indica* x *indica* hybrids of Silewah was substantial from both the *indica* and *japonica* stocks, suggesting their use in breeding.

Key words: Multivariate analysis, genetic diversity, cold-tolerant rice.

Reports on the use of multivariate analysis in selecting genetically divergent parents for a successful cold-tolerance breeding programme in rice are not available. A multivariate analysis of divergence was therefore carried out using Mahalanobis' D^2 static [1] for five quantitative characters related to reproductive stage cold tolerance and adaptability of *indica* and *japonica* rice strains and their hybrids in three diverse cold stress environments in South and Southeast Asia.

MATERIALS AND METHODS

Six high yielding *indica* type elite IRRI lines of rice were crossed as male parents with eight *japonica* and seven *indica* cultivars and elite lines having low-temperature tolerance at different growth stages in a line x tester design. The 90 F$_1$ hybrids and their 21 parents were

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*Present address: A1, Ligoury Court Apartments, No. 7, Palm Grove Road, Bangalore 560047.

transplanted in single row plots, 15 hills/row, replicated thrice, in a randomized block design at three locations.

The 15 female parents (Table 1) were selected for ecogeographic diversity, and originated from China (Leng Kwang and Shoa-Nan-Tsan), India (K39-96-3-1-1-1-2, Barkat, K 84, K 332 and China 988), Indonesia (Silewah), Japan (Shimokita), Korea (SR 3044-78-3, SR 5204-91-4-1, Suweon 235, Suweon 287 and Samgangbyeo) and USSR (Stejaree 45). While the

Table 1. Clustering pattern of 94 rice genotypes based on D^2 statistics

Cluster	No. of genotypes	Parent/hybrid
I	1	105
II	1	104
III	1	102 x 92
IV	12	103, 97, 108, 98, 99, 101, 100 x 92, 92, 98 x 94, 110, 98 x 93, 98 x 92
V	14	100 x 95, 98 x 95, 91, 98 x 91, 100 x 91, 100 x 94, 100, 111, 102, 103 x 92, 98 x 96, 100 x 96, 100 x 93, 102 x 94
VI	2	94, 103 x 94
VII	4	107, 107 x 94, 93, 103 x 93
VIII	7	96, 103 x 96, 102 x 96, 107 x 96, 107 x 93, 106 x 94, 106 x 91
IX	3	106, 106 x 95, 109
X	6	99 x 96, 110 x 96, 111 x 96, 109 x 95, 106 x 93, 106 x 96
XI	3	111 x 96, 105 x 96, 108 x 96
XII	4	107 x 92, 99 x 95, 106 x 92, 102 x 93
XIII	6	99 x 94, 104 x 96, 110 x 94, 111 x 93, 101 x 93, 111 x 94
XIV	15	108 x 95, 105 x 95, 104 x 95, 110 x 95, 99 x 92, 108 x 92, 108 x 91, 104 x 91, 99 x 91, 101 x 92, 108 x 94, 108 x 93, 111 x 92, 110 x 91, 99 x 93
XV	5	111 x 91, 104 x 94, 105 x 94, 104 x 93, 110 x 93
XVI	5	105 x 92, 104 x 92, 110 x 92, 105 x 91, 105 x 93
XVII	3	109 x 92, 109 x 91, 109 x 93
XVIII	2	109 x 94, 109 x 96

Japonica lines: Suweon 235 (97); SR 5204 (99); SR 3044 (101); Barket (104); K 332 (105); Shimokita (108); Stejaree 45 (110) and K 84 (111).

Indica lines: Suweon 287 (98); Samgangbyeo (100); China 988 (102); K 39-96 (103); Leng Kwang (106); Shoa-Nan-Tsan (107) and Silewah (109).

Indica testers: IR 8866 (91); IR 8455-K_2 (92); IR 15889 (93); IR 7167 (94); IR 29506 (95) and IR 9202 (96).

lines Barkat, K 84, K 332, Shimokita, SR 3044, SR 5204, Suweon 235 and Stejaree 45 (*japonica*) had high vegetative stage cold tolerance, the lines Leng Kwang, Shoa-Nan-Tsan, K 39-96, China 988, Silewah, Suweon 287 and Samgangbyeo (*indica*) had high reproductive stage cold tolerance. The six male parents crossed with each of the 15 females were IR 8866-30-3-1-4, IR 8455-K_2, IR 15889-32-1, IR 7167-33-2-3, IR 29506-60-3-3-2 and IR 9202-10-2-1-5-1. These were selected for high reproductive stage cold tolerance and high fertility.

The genotypes were evaluated for cold stress at Chuncheon (Korea), Upper Swat (Pakistan) and Banaue (Philippines) as described earlier [2]. Since some genotypes did not flower/mature at one or more of these locations, data on 74 hybrids (38 *japonica* x *indica* and 36 *indica* x *indica*) and 20 parents (15 females and 5 males) only were subjected to multivariate analysis using pooled data over the three environments. The genotypes were grouped into clusters according to Tocher's method (cf. [1]).

RESULTS AND DISCUSSION

Pooled analysis of variance revealed that the mean difference between genotypes and the environments for all the five characters studied were highly significant.

Using Wilk's Δ criterion (cf. [1]), the dispersion analysis revealed highly significant differences ($\chi^2 = 6829.4$ for 465 d.f.) among genotypes for the aggregate of the five correlated variables.

The D^2 values computed for all possible 4371 pairs of genotypes ranged from 0.7 in the crosses Shimokita x IR 8866 and Shimokita x IR 8455 to 907.9 in K 332 and Silewah x IR 9202. The 94 genotypes were grouped into 18 constellations based on D^2 statistic (Table 1, Fig. 1). Cluster XIV accommodated the highest number of genotypes (15), followed by cluster V (14) and cluster IV (12). While clusters I, II and III had one genotype each, clusters VI and XVIII had 2 genotypes each, and clusters IX, XI and XVII had 3 genotypes each.

The position of clusters appeared to be somewhat related to the parentage of cultures included. However, the six hybrids obtained by crossing the 6 testers with a single female line did not necessarily group in one cluster, suggesting genetic dissimilarity of the *indica* testers used. Traditional *japonica* type populations were clearly separated from the *indica* type in cluster formation. While the clusters XI, XIII, XIV, XV and XVI were exclusively formed by the *japonica* x *indica* hybrids (34 out of 38), clusters III, V, VI, VII, VIII and IX had *indica* x *indica* hybrids and indica parents, with a single *japonica* parent (K 84) located in cluster V. Clusters XV and XVI had hybrids of K 84 (111), Barkat (04) and K 332 (105) (all *japonica* strains from Kashmir) and Stejaree 45 (110) from USSR, suggesting common parentage in their pedigree. These cultures have vegetative stage cold tolerance genes

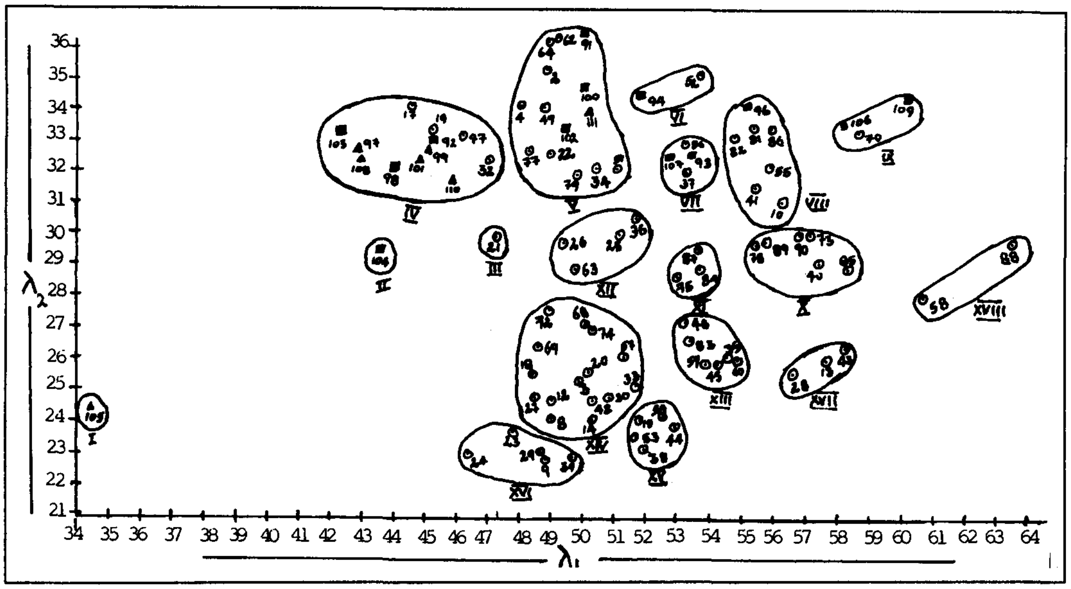

Fig. 1. **Group constellations of 94 rice genotypes in λ_1-λ_2 chart. Parental culture numbers correspond to Table 1. Triangles and squares represent japonica and indica parents, respectively.**

incorporated from japonica rice and are reported to have a high level of vegetative stage cold tolerance (cf. [2]).

The intracluster D^2 values ranged from 37.6 (cluster XI) to 8.3 (clusters VI and XIII), suggesting close genetic association inter se in the clusters VI and XIII. The intercluster divergence was maximum between clusters I and XVIII (823.3), both of which were also highly divergent from the remaining groups. Clusters I and IX were the next most divergent groups (746.5) and clusters XIII and XV were the closest (21.3). Cluster XVIII consisting of two Silewah hybrids was farthest from other clusters, followed by cluster XVII, also housing three other hybrids of Silewah. Silewah thus appears to have a distinctly divergent pedigree compared to other *indica* lines. Cluster I formed by the sole *japonica* variety, K 332, was also highly divergent and distinctly isolated. Cluster XVIII, which was based on two *indica* x *indica* hybrids of Silewah, and cluster IX on two *indica* parents, Leng Kwang and Silewah, and the *indica* x *indica* hybrid Leng Kwang x IR 29506 appear to have a close genetic association. This could be expected as both Silewah and Leng Kwang are tall varieties with long panicle, bred for the specific purpose of panicle harvesting, and have similar flowering duration, plant height, panicle length, fertility level, and cold tolerance [3].

The overall contribution of the first two canonical roots to total variability among the 94 populations accounted for 78.5% of total variability (45.9% by λ_1 and 32.6% by λ_2), suggesting completion of a major portion of differentiation in the first two phases. The relative distribution of genotypes (Fig. 1) reflects a broad parallelism between the groupings obtained by D^2 analysis and canonical analysis. Divergences between clusters I and XVIII, and I and IX were distinctly delineated as in D^2 analysis.

From the absolute magnitude of the coefficients of the first two canonical vectors Z_1 and Z_2, plant height (0.76), followed by days to flowering (0.54) and panicle length (0.30) in the primary axis of differentiation and fertile spikelet number (0.70), followed by fertility (0.48) and days to flowering (0.47), in the secondary axis of differentiation were important contributors to genetic divergence of cold tolerant rices in this set of genotypes. Flowering time, 1000-grain weight and plant height were reported to have made important contributions to genetic divergence in 26 photoperiod-insensitive rice varieties grown under Assam climate [4]. According to Oka [5], rice cultivars exhibit, in addition to their differentiation into the *japonica* and *indica* types, a spectrum of character differences in morphology, physiological responses, hybrid sterility relationships, and agronomic capacities.

A marked intracluster variation in the cluster means for all the characters (Table 2), highlights their role in the differentiation. Cluster pairs I–XVIII and I–IX were extremely divergent with regard to days to flowering, plant height, panicle length and fertility, which accounts for their intercluster divergence, as reported earlier. The clusters XIII, XIV, XV and XVI having only *japonica* x *indica* hybrids have shown lower fertility and fertile spikelets/panicle as compared to clusters III, V, VI, VII, VIII and IX which comprised *indica* parents and *indica* x *indica* hybrids, and had relatively higher fertility and fertile spikelets per panicle. Clusters VI (IR 7167, K 39-96 x IR 7167) and VII (Shoa-Nan-Tsan, IR

Table 2. Cluster means of five characters in 94 rice genotypes

Cluster	Days to flower	Plant height (cm)	Panicle length (cm)	Fertile spikelets per panicle	Fertility (%)
I	**73.8***	**78.1***	**16.1***	60.0	72.0
II	95.5	96.6	16.9	79.5	71.4
III	97.1	106.7	23.0	88.3	70.8
IV	101.3	85.9	20.3	90.7	**77.7****
V	110.8	94.1	22.2	97.5	70.2
VI	115.5	106.0	22.9	**108.5****	68.5
VII	108.7	121.5	24.3	107.0	69.6
VIII	115.4	121.1	24.9	91.8	59.0
IX	**125.1****	125.5	24.5	79.2	52.3
X	112.8	133.1	25.1	72.2	45.3
XI	108.8	118.9	23.9	71.0	43.2
XII	103.5	113.6	23.2	81.5	58.4
XIII	106.6	126.7	23.9	44.3	32.6
XIV	103.3	104.2	22.4	36.8	26.0
XV	101.1	124.5	23.3	34.3	24.0
XVI	97.7	105.4	21.7	**27.5***	**20.0***
XVII	109.8	139.0	27.3	40.7	27.3
XVIII	120.4	**144.9****	**28.6****	51.6	28.9
Mean	107.0	110.0	23.0	69.5	50.0
SE ±	1.1	2.4	0.5	5.1	3.0

*,**Minimum and maximum mean values, respectively.

15889, Shoa-Nan-Tsan x IR 7167, K 39-96 x IR 15889), however, combined all the good attributes for reproductive stage cold tolerance, including plant height. Cluster I (K 332), on the other hand, flowered early, had short plant stature and smaller panicles like the typical *japonica* rices, but had higher number of fertile spikelets/panicle and high fertility like the *indica* rices. Clausen and Hiesey [6] have demonstrated that even a single component of environment, such as temperature, could cause differences between and within races. Similar factors appeared to have played a part in the divergence of *indica* and *japonica* rices. Irrespective of the geographical regions to which they belonged, the *japonica* rices were distinctly delineated from the *indica* rices in the present study.

The main reasons for the interstrain diversity of cold tolerant *japonica* and *indica* rices could thus be attributed to genetic drift and application of different selection criteria, like selection for high level of vegetative stage cold tolerance in *japonica* rice, which is subjected to cold irrigation water throughout the growing season, and selection for a desirable plant type with high productivity and quality under good management in *indica* rice. According to Anderson [7], the separation of two populations for a long time could cause greater divergence under selection for homozygotes.

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